This amendment contains no new matter. The amendments to the specification and/or claims are to provide a formal sequence listing and/or to provide appropriate cross-references to SEQ ID Numbers in accordance with 37 C.F.R. §§1.821 to 1.825. The sequence information provided herein finds support in the specification as filed.

If a telephone conference would expedite prosecution of this application, the Examiner is invited to telephone the undersigned at (510) 337-7871.

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Respectfully submitted,

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APPENDIX A

VERSION WITH MARKINGS TO SHOW CHANGES MADE IN 10/028,056 WITH ENTRY OF THIS AMENDMENT

In the specification:

Paragraph 158, page 45:

[0158] The sequence requirement for the hairpin ribozyme is any RNA sequence consisting of nnnbn*gucnnnnnn (where N*G is the cleavage site, where B is any of G, C, or U, and where N is any of G, U, C, or A) (SEQ ID NO:**12** [___]). Suitable lipin of recognition or target sequences for hairpin ribozymes can be readily determined from the lipin sequence(s) identified herein.

Paragraph 203, page 60:

[**0203**] Mouse genomic DNA was prepared using DNAzol (Gibco/BRL). Blots containing restriction digested DNA (5 μg/lane) were hybridized to a 257-bp 5' probe corresponding to exons 2 and 3 derived from exon trapping (Péterfy *et al.* (1999) *Genomics* 62: 436-444), or a 225-bp 3' probe corresponding to part of the 3' UTR and generated by PCR (5'-TAC GCA GGG ACA CAT TTC CA-3', SEQ ID NO:**13**[_]) and 5'-GAG AGA TGC AGC TGC GTC A-3', SEQ ID NO: **14**[_]). Hybridizations were performed at 65°C in 0.5 M sodium phosphate, pH 7.0, 7% SDS, 1% BSA, and washed at 65°C to a final stringency of 0.1X SSC/ 0.1% SDS. Hybridization signals were detected by phosphorimaging.

Paragraph 205, pages 60-61:

[0205] PCR amplification of genomic DNA was performed in an M/J Research PTC-200 thermocycler (1 min 94°C, 45 sec 55°C, 1-2 min 72°C) for 30-32 cycles. Primers for amplification of the inversion breakpoints (Fig. 2*b*) were: p1, 5'-CCC TTG AGC ACG TTC ACA-3' (SEQ ID NO: **15**[_]); p2, 5'-CTG ATC GTT GTC AGT CTC T-3' (SEQ ID NO: **16**[_]); p3, 5'-GGT TGT GGG GAC CCT GGA-3' (SEQ ID NO: **17**[_]); p4, 5'-GCC TGC TGC AGA TGC GTT-3' (SEQ ID NO: **18**[_]). RACE cloning of full length cDNAs for *Lpin2* and *Lpin3* was performed using liver

cDNA template prepared with the Marathon cDNA Amplification Kit (Clontech). PCR products were TA-cloned into pCR2.1 (Invitrogen), and sequenced using the Amplicycle sequencing kit (Perkin Elmer) and an ABI model 373A sequencer.

Paragraph 206, page 61:

[**0206**] The entire coding region of the lipin cDNA was amplified from liver cDNA using the primers 5'-GCT CGA ATT CAG ACA ATG AAT TAC GTG GGG CAG CT-3' (SEQ ID NO: **19**[_]) and 5'-CGT GCA GTC GAC GCT GAG GCT GAA TGC ATG TCC TGG T-3' (SEQ ID NO: **20**[_]) and cloned as an *Eco*RI/*Sal*I fragment into the pEGFP-N1 vector (Clontech). 3T3-L1 cells were transfected using Lipofectin (Gibco/BRL). 48 hours after transfection, cells were fixed with 4% paraformaldehyde in PBS, stained with Hoechst-33258 dye, and observed with a Zeiss Axiophot fluorescence microscope.

Paragraph 208, page 61:

[**0208**] *Lpin2* and *Lpin3* were mapped using a mouse-hamster radiation hybrid panel (Research Genetics) (McCarthy *et al.* (1997) *Genome Res.* 7: 1153-1161). Oligonucleotide primer pairs derived from the 3'UTR of each gene were as follows: *Lpin2* (5-GGC GAG ACC CAA TCC CTG A-3', SEQ ID NO: **21**[_]) and 5'-GGG TCT TCC TCT GTA AGA-3', SEQ ID NO: **22**[_]); *Lpin3* (5'-CCT GGC TTG AGC TTG CCT T-3', SEQ ID NO: **23**[_], and 5'-CCC ACG GCA TGC ATC TTC T-3', SEQ ID NO: **24**[_]).

Paragraph 217, page 63:

[**0217**] The N-LIP and acidic lipin protein domains are required for nuclear localization (Figures **Error! Reference source not found.** and **Error! Reference source not found.**). Initial studies of lipin localization within the cell revealed that lipin occurs as a predominantly nuclear protein, with a small, but consistent number of cells that exhibit exclusively cytoplasmic localization. Lipin contains a putative nuclear localization signal (NLS) comprised of basic amino acids (KKRRKRRK, SEQ ID NO: **25**[_]).